SEQUENCE LISTING

<110>   Sanjay Bhanot
Kenneth W. Dobie

<120>   MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION

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                                                           Met Lys
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acc ctc ata gcc gcc tac tcc ggg gtc ctg cgc ggc gag cgt cag gcc        284
Thr Leu Ile Ala Ala Tyr Ser Gly Val Leu Arg Gly Glu Arg Gln Ala
            5               10                  15

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Glu Ala Asp Arg Ser Gln Arg Ser His Gly Gly Pro Ala Leu Ser Arg
        20                  25                  30

gag ggg tct ggg aga tgg ggc act gga tcc agc atc ctc tcc gcc ctc        380
Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser Ile Leu Ser Ala Leu
35                  40                  45                  50

cag gac ctc ttc tct gtc acc tgg ctc aat agg tcc aag gtg gaa aag        428
Gln Asp Leu Phe Ser Val Thr Trp Leu Asn Arg Ser Lys Val Glu Lys
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Gln Leu Gln Val Ile Ser Val Leu Gln Trp Val Leu Ser Phe Leu Val
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ctg gga gtg gcc tgc agt gcc atc ctc atg tac ata ttc tgc act gat        524
Leu Gly Val Ala Cys Ser Ala Ile Leu Met Tyr Ile Phe Cys Thr Asp
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tgc tgg ctc atc gct gtg ctc tac ttc act tgg ctg gtg ttt gac tgg        572
Cys Trp Leu Ile Ala Val Leu Tyr Phe Thr Trp Leu Val Phe Asp Trp
100                 105                 110

aac aca ccc aag aaa ggt ggc agg agg tca cag tgg gtc cga aac tgg        620
Asn Thr Pro Lys Lys Gly Gly Arg Arg Ser Gln Trp Val Arg Asn Trp
115                 120                 125                 130

gct gtg tgg cgc tac ttt cga gac tac ttt ccc atc cag ctg gtg aag        668
Ala Val Trp Arg Tyr Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys
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aca cac aac ctg ctg acc acc agg aac tat atc ttt gga tac cac ccc        716
Thr His Asn Leu Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro
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cat ggt atc atg ggc ctg ggt gcc ttc tgc aac ttc agc aca gag gcc        764
His Gly Ile Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala
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aca gaa gtg agc aag aag ttc cca ggc ata cgg cct tac ctg gct aca        812
Thr Glu Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr
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ctg gca ggc aac ttc cga atg cct gtg ttg agg gag tac ctg atg tct        860
Leu Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser
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gga ggt atc tgc cct gtc agc cgg gac acc ata gac tat ttg ctt tca        908
Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu Ser
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Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr Leu Arg Asn
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cgc aag ggc ttt gtg aaa ctg gcc ctg cgt cat gga gct gac ctg gtt    1052
Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly Ala Asp Leu Val
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ccc atc tac tcc ttt gga gag aat gaa gtg tac aag cag gtg atc ttc    1100
Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr Lys Gln Val Ile Phe
275              280                  285              290

gag gag ggc tcc tgg ggc cga tgg gtc cag aag aag ttc cag aaa tac    1148
Glu Glu Gly Ser Trp Gly Arg Trp Val Gln Lys Lys Phe Gln Lys Tyr
            295              300              305

att ggt ttc gcc cca tgc atc ttc cat ggt cga ggc ctc ttc tcc tcc    1196
Ile Gly Phe Ala Pro Cys Ile Phe His Gly Arg Gly Leu Phe Ser Ser
            310              315              320

gac acc tgg ggg ctg gtg ccc tac tcc aag ccc atc acc act gtt gtg    1244
Asp Thr Trp Gly Leu Val Pro Tyr Ser Lys Pro Ile Thr Thr Val Val
        325              330                  335

gga gag ccc atc acc atc ccc aag ctg gag cac cca acc cag caa gac    1292
Gly Glu Pro Ile Thr Ile Pro Lys Leu Glu His Pro Thr Gln Gln Asp
        340              345                  350

atc gac ctg tac cac acc atg tac atg gag gcc ctg gtg aag ctc ttc    1340
Ile Asp Leu Tyr His Thr Met Tyr Met Glu Ala Leu Val Lys Leu Phe
355              360                  365              370

gac aag cac aag acc aag ttc ggc ctc ccg gag act gag gtc ctg gag    1388
Asp Lys His Lys Thr Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu
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gtg aac tga gccagccttc ggggccaact ccctggagga accagctgca aatcactttt  1447
Val Asn

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gtggctcagc taacctctct tcttcccttc ctgaagtgac aaaggaaact cagtcttctt  1687

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Gly Val Leu Arg Gly Glu Arg Arg Ala Glu Ala Ala Arg Ser Glu Asn
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Lys Asn Lys Gly Ser Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly
                30              35                  40

act ggc tcc agc atc ctc tca gcc ctc caa gac atc ttc tct gtc acc    377
Thr Gly Ser Ser Ile Leu Ser Ala Leu Gln Asp Ile Phe Ser Val Thr
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Trp Leu Asn Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val
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cta caa tgg gtc cta tcc ttc ctg gtg cta gga gtg gcc tgc agt gtc    473
Leu Gln Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Val

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tac ttc acc tgg ctg gca ttt gac tgg aac acg ccc aag aaa ggt ggc      569
Tyr Phe Thr Trp Leu Ala Phe Asp Trp Asn Thr Pro Lys Lys Gly Gly
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agg aga tcg cag tgg gtg cga aac tgg gcc gtg tgg cgc tac ttc cga      617
Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr Phe Arg
             125                 130                 135

gac tac ttt ccc atc cag ctg gtg aag aca cac aac ctg ctg acc acc      665
Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu Leu Thr Thr
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Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile Met Gly Leu Gly
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gcc ttc tgt aac ttc agc aca gag gct act gaa gtc agc aag aag ttt      761
Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu Val Ser Lys Lys Phe
170             175                 180                 185

cct ggc ata agg ccc tat ttg gct acg ttg gct ggt aac ttc cgg atg      809
Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu Ala Gly Asn Phe Arg Met
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cct gtg ctt cgc gag tac ctg atg tct gga ggc atc tgc cct gtc aac      857
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cga gac acc ata gac tac ttg ctc tcc aag aat ggg agt ggc aat gct      905
Arg Asp Thr Ile Asp Tyr Leu Leu Ser Lys Asn Gly Ser Gly Asn Ala
             220                 225                 230

atc atc atc gtg gtg gga ggt gca gct gag tcc ctg agc tcc atg cct      953
Ile Ile Ile Val Val Gly Gly Ala Ala Glu Ser Leu Ser Ser Met Pro
             235                 240                 245

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Gly Lys Asn Ala Val Thr Leu Lys Asn Arg Lys Gly Phe Val Lys Leu
250             255                 260                 265

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Ala Leu Arg His Gly Ala Asp Leu Val Pro Thr Tyr Ser Phe Gly Glu
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aat gag gta tac aag cag gtg atc ttt gag gag ggt tcc tgg ggc cga      1097
Asn Glu Val Tyr Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg
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tgg gtc cag aag aag ttc cag aag tat att ggt ttc gcc ccc tgc atc      1145
Trp Val Gln Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile
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ttc cat ggc cga ggc ctc ttc tcc tct gac acc tgg ggg ctg gtg ccc      1193
Phe His Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro
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Tyr Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Val Pro
330             335                 340                 345
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tac atg gag gcc ctg gtg aag ctc ttt gac aat cac aag acc aaa ttt      1337
Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Asn His Lys Thr Lys Phe
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ggc ctt cca gag act gag gtg ctg gag gtg aac tga cccagccctc          1383
Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn
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